SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Boynton, John E.
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(ii) TITLE OF INVENTION: Methods of Conferring PPO-Inhibiting Herbicide Resistance to Plants by Gene Manipulation

(iii) NUMBER OF SEQUENCES: 24

(iv) CORRESPONDENCE ADDRESS:
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patentin Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US new
(B) FILING DATE: 30-SEP-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Murphy Jr., Gerald M.
(B) REGISTRATION NUMBER: 28,977
(C) REFERENCE/DOCKET NUMBER: 2185-156P

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chlamydomonas reinhardtii*
(B) STRAIN: CC-407

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..47
(D) OTHER INFORMATION: /product= "porphyric herbicide resistance domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Ala Glu Ala Leu Gly Ser Phe Asp Tyr Pro Pro Val Gly Ala Val
1 5 10 15

Thr Leu Ser Tyr Pro Leu Ser Ala Val Arg Glu Glu Arg Lys Ala Ser
20 25 30

Asp Gly Ser Val Pro Gly Phe Gly Gln Leu His Pro Arg Thr Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Arabidopsis thaliana*
(B) STRAIN: ecotype Columbia

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..46
(D) OTHER INFORMATION: /product= "porphyric herbicide resistance domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val
1 5 10 15

Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp
20 25 30

Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Zea mays*
(B) STRAIN: B73 inbred

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..46
(D) OTHER INFORMATION: /product= "porphyric herbicide resistance domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Ala Asp Ala Leu Ser Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val
1 5 10 15

Thr Val Ser Tyr Pro Lys Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp
20 25 30

Gly Glu Leu Gln Gly Phe Gly Gln Leu His Pro Arg Ser Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chlamydomonas reinhardtii*
(B) STRAIN: CC-407

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..141
(D) OTHER INFORMATION: /note= "encodes porphyric herbicide resistance domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCGCCGAGG CCCTGGGCTC CTTCGACTAC CCGCCGGTGG GCGCCGTGAC GCTGTCGTAC 60

CCGCTGAGCG CCGTGCGGGA GGAGCGCAAG GCCTCGGACG GGTCCGTGCC GGGCTTCGGT 120

CAGCTGCACC CGCGCACGCA G 141

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Arabidopsis thaliana*
(B) STRAIN: ecotype Columbia

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..138
(D) OTHER INFORMATION: /note= "encodes porphyric herbicide resistance domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTGCAAATG CACTCTCAAA ACTATATTAC CCACCAGTTG CAGCAGTATC TATCTCGTAC 60

CCGAAAGAAG CAATCCGAAC AGAATGTTTG ATAGATGGTG AACTAAAGGG TTTTGGGCAA 120

TTGCATCCAC GCACGCAA 138

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Zea mays*
(B) STRAIN: B73 inbred

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..138
(D) OTHER INFORMATION: /note= "encodes porphyric herbicide resistance domain"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCTGCAGATG CTCTATCAAG ATTCTATTAT CCACCGGTTG CTGCTGTAAC TGTTTCGTAT 60

CCAAAGGAAG CAATTAGAAA AGAATGCTTA ATTGATGGGG AACTCCAGGG CTTTGGCCAG 120

TTGCATCCAC GTAGTCAA 138

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: NO
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..36
(C) OTHER INFORMATION:/NOTE = "oligonucleotide primer for *Arabidopsis thaliana*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTATATTACC CACCAATGGC AGCAGTATCT ATCTCG 36

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: "oligonucleotide"

(iii) HYPOTHETICAL: NO
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..38
(C) OTHER INFORMATION:/NOTE = "oligonucleotide primer for *Zea mays*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATTCTATTA TCCACCGATG GCTGCTGTAA CTGTTTCG 38

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: "oligonucleotide"

(iii) HYPOTHETICAL: YES

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /note= "oligonucleotide primer common to both of A. thaliana and Z. mays porphyric herbicide resistance domain of PPO."
/note= "N residues can be inosine (I) in addition to G, A, T or C. K = G or T, Y = C or T, S = C or G, W = A or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

KAYTAYCCNC CNATGGSNGC NGTNWS 26

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULAR TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chlamydomonas reinhardtii*
(B) STRAIN: RS-3

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..2573

(C)OTHER INFORMATION:/note="encodes protoporphyrinogen oxidase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTCGAGAGCG TTGGAGGAAA TCCGTTTGGC ACCTGTTCCG GCTTCTTTGT GTGCACGGCC 60

ACGTCCCCCT TTCCTGCTAC CCGCTCCCCC CCGGCTTTAC TGCCCCTTCC ACTCCTCGGC 120

TCCATCCCGA TTCCATCCGC TCCTCCTCCC CCACCTAGAC TGTCTACCGT CTACCAGTTT 180

CTTGGGCAAT CATTAACGTA ACCCCGCCTC CCTGCGCCTG CCCCTCCCTC CCTCTCCCCC 240

CCGCACAGCC CGCCGCCGCC GAGGCCCTGG GCTCCTTCGA CTACCCGCCG ATGGGCGCCG 300

TGACGCTGTC GTACCCGCTG AGCGCCGTGC GGGAGGAGCG CAAGGCCTCG GACGGGTCCG 360

TGCCGGGCTT CGGTCAGCTG CACCCGCGCA CGCAGGTGGG CAAGTGCGCG CGTGTTGCGG 420

GCGGTGTGTT GCGGAGGGGA GGGTGGTGGG GGTTGGGGGT GGGGGTGGGG GGGATTGGGG 480

CGCTGGGTCG TATCCCGCGG TTGTATCCTC GCGCTCCCCT CATCCATTCC CCCCTTCAAC 540

AACACACACG GGCGCACACG CACCCTCTTT GCGCTTACTT TGTCTGGTGC TCCTTAACAC 600

ACTCTTCGCT TCATTTTGGT GTCTTCTAAC ACACACACTT GTCCACACAC AGGGCATCAC 660

CACTCTGGGC ACCATCTACA GCTCCAGCCT GTTCCCCGGC CGCGCGCCCG AGGGCCACAT 720

GCTGCTGCTC AACTACATCG GCGGCACCAC CAACCGCGGC ATCGTCAACC AGACCACCGA 780

GCAGCTGGTG GAGCAGGTGT GTGTGTGGGG GGGTGGGGGG GGGGCAGTGG ATTTTTGGGC 840

TGAGCCCCCT GAGCAAAGCG ATCCAGGGGG GGCGAAGCCC CCCAGGATTG CCCCTGTCCG 900

TGCGTGCGTG TGTGCCTGTG TCGACAAAAA GTACCGTACT GGCACAAACC GCGAGTGCCA 960

CGTATTATTA ATTGCAATTA CCTATTGTAG AAAAATAGAC GGCAGGGAAA ACTCGGCCGG 1020

AGCGAGAAGC GACCTCGTGA GTCCATGGAC ATCTTGACTT TCTTCAGTTC GCGAGTATAG 1080

CTCTCGGCCC CTAAATATCT TACATCCATG TATCAAAACA TGTCGACGAC AAGCGTCTTG 1140

GGGCAAGAAT GTCGAAATTG TTTGCAACAG CCAAACCATG CGTCCCCGAG CCTTACATGT 1200

GTCGCGGCCC GGGATCCCGC GCCCGAGCCC GGCTAGCCCT TTGCGGTGCT TGAGTGGGAT 1260

GTGGGTGAGG TGCATTTGGG ATATCATGGA CCGTGAAGTG GCGTGGGTAA GGTGGCGTGG 1320

CGTGGCGGGG ACAGGGCATG TCGGTGCCTC GGCACAGCGT TGGCCTAGTG GCCAGTCCCG 1380

CTGGATGGGC TTGCAAGGGT GCTGTTCATG TCGCCGGTGC CCATCGTCAC ATCCCCTTGC 1440

GCTACATGGG GCTCAGCCCA TTTTCCAGCT GTACAAAGCT GACACCCCTT GTTGTGTGGC 1500

GTCTTGGACC CGTGTTGCTT CGGAGCTGGC CAGAACCCCC TGTGGGCACA CACACGCACA 1560

CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA 1620

CACACACACA CACACACACA CACACACACA CACACACACA CACATTTTCG TCCTGCAGCC 1680

CCGAACCCCG CCGCCCGTTC CACGTCTTCC ACCTGCCGCA CCCCCCCCCC TGCCGCACGC 1740

CTGCTCTCAC CGCCTCTCCC CCCACCCCAT CTCCCTGCAG GTGGACAAGG ACCTGCGCAA 1800

CATGGTCATC AAGCCCGACG CGCCCAAGCC CCGTGTGGTG GGCGTGCGCG TGTGGCCGCG 1860

CGCCATCCCG CAGGTGTGAG GGCGCAGCAG CCGGAGGGAT GGGCTAGATC CTAGTTTCTC 1920

AAAGAGCTCT ACAGCCCTAT AACCTCGACC TGCGACCTTC GACCTGATAA CCTGGCTGCC 1980

CCCTCCCAAC CTAGCCACCT CTCCCCGGAT TTGGGTTCAC TCGGTTGACT TGCTTTTGGG 2040

TTCTGGAATC AACTTCACCT GTTGTATACT TTGCTGCACT TCTCTGTACC ACTCTTTGCA 2100

TTAGGTTCGG TTTAGTTTGG GCTGCATGTG TAACCCCTCC TCCCCGCCCT GCCACCTGCA 2160

GTTCAACCTG GGCCACCTGG AGCAGCTGGA CAAGGCGCGC AAGGCGCTGG ACGCGGCGGG 2220

GCTGCAGGGC GTGCACCTGG GGGGCAACTA CGTCAGCGGT GAGCGCGTGG GCAGCAGCAG 2280

CAGCAGGAAG AGGGGAGGGG AGGGGAGGGG AGGGTACAAG GAGGAGGTTG AGCAGGAGGT 2340

GGTGCTAAGG CGCAAAGCAA GGCGGTGTTG TATCCTCATT GACTGAAACC GGGAAACCCA 2400

GCATGAACAA GAGGTCAGGG GACTGCAAGG AGCGGAGGCT ACATGTATGA CTACCCCCGA 2460

CGCGGGCGAT GATTCCTTGA CTATTGGGAC CTATTTCGTT GGGCTCGGGC ACATGACCCC 2520

CCTGGCCCCT TCGCTGTATG GTGCCCAGCC GCCCAGCCGC CCCCCGCCCA CAC 2573

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1704 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Arabidopsis thaliana*
(B) STRAIN: ecotype Columbia

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 16..1629
(D) OTHER INFORMATION: /product= "protoporphyrinogen oxidase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
TTCTCTGCGA TTTCC ATG GAG TTA TCT CTT CTC CGT CCG ACG ACT CAA TCG      51
                 Met Glu Leu Ser Leu Leu Arg Pro Thr Thr Gln Ser
                   1               5                  10

CTT CTT CCG TCG TTT TCG AAG CCC AAT CTC CGA TTA AAT GTT TAT AAG      99
Leu Leu Pro Ser Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys
          15                  20                  25

CCT CTT AGA CTC CGT TGT TCA GTG GCC GGT GGA CCA ACC GTC GGA TCT     147
Pro Leu Arg Leu Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser
      30                  35                  40

TCA AAA ATC GAA GGC GGA GGA GGC ACC ACC ATC ACG ACG GAT TGT GTG     195
Ser Lys Ile Glu Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val
  45                  50                  55                  60

ATT GTC GGC GGA GGT ATT AGT GGT CTT TGC ATC GCT CAG GCG CTT GCT     243
Ile Val Gly Gly Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala
                  65                  70                  75

ACT AAG CAT CCT GAT GCT GCT CCG AAT TTA ATT GTG ACC GAG GCT AAG     291
Thr Lys His Pro Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys
              80                  85                  90

GAT CGT GTT GGA GGC AAC ATT ATC ACT CGT GAA GAG AAT GGT TTT CTC     339
Asp Arg Val Gly Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu
          95                  100                 105

TGG GAA GAA GGT CCC AAT AGT TTT CAA CCG TCT GAT CCT ATG CTC ACT     387
Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr
      110                 115                 120

ATG GTG GTA GAT AGT GGT TTG AAG GAT GAT TTG GTG TTG GGA GAT CCT     435
Met Val Val Asp Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro
  125                 130                 135                 140

ACT GCG CCA AGG TTT GTG TTG TGG AAT GGG AAA TTG AGG CCG GTT CCA     483
Thr Ala Pro Arg Phe Val Leu Trp Asn Gly Lys Leu Arg Pro Val Pro
                  145                 150                 155

TCG AAG CTA ACA GAC TTA CCG TTC TTT GAT TTG ATG AGT ATT GGT GGG     531
Ser Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly Gly
              160                 165                 170

AAG ATT AGA GCT GGT TTT GGT GCA CTT GGC ATT CGA CCG TCA CCT CCA     579
Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro
          175                 180                 185

GGT CGT GAA GAA TCT GTG GAG GAG TTT GTA CGG CGT AAC CTC GGT GAT     627
Gly Arg Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp
      190                 195                 200

GAG GTT TTT GAG CGC CTG ATT GAA CCG TTT TGT TCA GGT GTT TAT GCT     675
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Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala
205                 210                 215                 220

GGT GAT CCT TCA AAA CTG AGC ATG AAA GCA GCG TTT GGG AAG GTT TGG     723
Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp
                225                 230                 235

AAA CTA GAG CAA AAT GGT GGA AGC ATA ATA GGT GGT ACT TTT AAG GCA     771
Lys Leu Glu Gln Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala
            240                 245                 250

ATT CAG GAG AGG AAA AAC GCT CCC AAG GCA GAA CGA GAC CCG CGC CTG     819
Ile Gln Glu Arg Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu
        255                 260                 265

CCA AAA CCA CAG GGC CAA ACA GTT GGT TCT TTC AGG AAG GGA CTT CGA     867
Pro Lys Pro Gln Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg
    270                 275                 280

ATG TTG CCA GAA GCA ATA TCT GCA AGA TTA GGT AGC AAA GTT AAG TTG     915
Met Leu Pro Glu Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu
285                 290                 295                 300

TCT TGG AAG CTC TCA GGT ATC ACT AAG CTG GAG AGC GGA GGA TAC AAC     963
Ser Trp Lys Leu Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn
                305                 310                 315

TTA ACA TAT GAG ACT CCA GAT GGT TTA GTT TCC GTG CAG AGC AAA AGT    1011
Leu Thr Tyr Glu Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser
            320                 325                 330

GTT GTA ATG ACG GTG CCA TCT CAT GTT GCA AGT GGT CTC TTG CGC CCT    1059
Val Val Met Thr Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro
        335                 340                 345

CTT TCT GAA TCT GCT GCA AAT GCA CTC TCA AAA CTA TAT TAC CCA CCA    1107
Leu Ser Glu Ser Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro
    350                 355                 360

GTT GCA GCA GTA TCT ATC TCG TAC CCG AAA GAA GCA ATC CGA ACA GAA    1155
Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu
365                 370                 375                 380

TGT TTG ATA GAT GGT GAA CTA AAG GGT TTT GGG CAA TTG CAT CCA CGC    1203
Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg
                385                 390                 395

ACG CAA GGA GTT GAA ACA TTA GGA ACT ATC TAC AGC TCC TCA CTC TTT    1251
Thr Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe
            400                 405                 410

CCA AAT CGC GCA CCG CCC GGA AGA ATT TTG CTG TTG AAC TAC ATT GGC    1299
Pro Asn Arg Ala Pro Pro Gly Arg Ile Leu Leu Leu Asn Tyr Ile Gly
        415                 420                 425

GGG TCT ACA AAC ACC GGA ATT CTG TCC AAG TCT GAA GGT GAG TTA GTG    1347
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Gly Ser Thr Asn Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val
    430                 435                 440

GAA GCA GTT GAC AGA GAT TTG AGG AAA ATG CTA ATT AAG CCT AAT TCG     1395
Glu Ala Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser
445                 450                 455                 460

ACC GAT CCA CTT AAA TTA GGA GTT AGG GTA TGG CCT CAA GCC ATT CCT     1443
Thr Asp Pro Leu Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro
                465                 470                 475

CAG TTT CTA GTT GGT CAC TTT GAT ATC CTT GAC ACG GCT AAA TCA TCT     1491
Gln Phe Leu Val Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser
            480                 485                 490

CTA ACG TCT TCG GGC TAC GAA GGG CTA TTT TTG GGT GGC AAT TAC GTC     1539
Leu Thr Ser Ser Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val
        495                 500                 505

GCT GGT GTA GCC TTA GGC CGG TGT GTA GAA GGC GCA TAT GAA ACC GCG     1587
Ala Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala
    510                 515                 520

ATT GAG GTC AAC AAC TTC ATG TCA CGG TAC GCT TAC AAG TAA             1629
Ile Glu Val Asn Asn Phe Met Ser Arg Tyr Ala Tyr Lys  *
525                 530                 535

ATGTAAAACA TTAAATCTCC CAGCTTGCGT GAGTTTTATT AAATATTTTG AGATATCCAA  1689

AAAAAAAAAA AAAAA                                                   1704
```

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH:537 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Arabidopsis thaliana*
- (B) STRAIN: ecotype Columbia

(ix) FEATURE:
- (A) NAME/KEY:Peptide
- (B) LOCATION:1..537
- (C) OTHER INFORMATION:/product="protoporphyrinogen oxidase"

(xi) SEQUENCE DESCRIPTION: SEQ. ID. NO:12:

```
Met Glu Leu Ser Leu Leu Arg Pro Thr Thr Gln Ser Leu Leu Pro Ser
  1               5                  10                  15
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Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys Pro Leu Arg Leu
20 25 30

Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser Ser Lys Ile Glu
35 40 45

Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val Ile Val Gly Gly
50 55 60

Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala Thr Lys His Pro
65 70 75 80

Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys Asp Arg Val Gly
85 90 95

Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu Trp Glu Glu Gly
100 105 110

Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Val Val Asp
115 120 125

Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Thr Ala Pro Arg
130 135 140

Phe Val Leu Trp Asn Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr
145 150 155 160

Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly Gly Lys Ile Arg Ala
165 170 175

Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro Gly Arg Glu Glu
180 185 190

Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp Glu Val Phe Glu
195 200 205

Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser
210 215 220

Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Gln
225 230 235 240

Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Gln Glu Arg
245 250 255

Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu Pro Lys Pro Gln
260 265 270

Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Glu
275 280 285

Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu Ser Trp Lys Leu
290 295 300

Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn Leu Thr Tyr Glu

```
305                 310                 315                 320

Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser Val Val Met Thr
                325                 330                 335

Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro Leu Ser Glu Ser
            340                 345                 350

Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val
        355                 360                 365

Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp
    370                 375                 380

Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val
385                 390                 395                 400

Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala
                405                 410                 415

Pro Pro Gly Arg Ile Leu Leu Leu Asn Tyr Ile Gly Gly Ser Thr Asn
            420                 425                 430

Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val Glu Ala Val Asp
        435                 440                 445

Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser Thr Asp Pro Leu
    450                 455                 460

Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val
465                 470                 475                 480

Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser Leu Thr Ser Ser
                485                 490                 495

Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ala Gly Val Ala
            500                 505                 510

Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala Ile Glu Val Asn
        515                 520                 525

Asn Phe Met Ser Arg Tyr Ala Tyr Lys  *
    530                 535
```

(2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1698 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULAR TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Zea mays*
(B) STRAIN: B73 inbred

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..1453
(C) OTHER INFORMATION: /product="protoporphyrinogen oxidase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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G AAT TCG GCG GAC TGC GTC GTG GTG GGC GGA GGC ATC AGT GGC CTC          46
  Asn Ser Ala Asp Cys Val Val Val Gly Gly Gly Ile Ser Gly Leu
    1               5                  10                  15

TGC ACC GCG CAG GCG CTG GCC ACG CGG CAC GGC GTC GGG GAC GTG CTT        94
Cys Thr Ala Gln Ala Leu Ala Thr Arg His Gly Val Gly Asp Val Leu
                20                  25                  30

GTC ACG GAG GCC CGC GCC CGC CCC GGC GGC AAC ATT ACC ACC GTC GAG       142
Val Thr Glu Ala Arg Ala Arg Pro Gly Gly Asn Ile Thr Thr Val Glu
            35                  40                  45

CGC CCC GAG GAA GGG TAC CTC TGG GAG GAG GGT CCC AAC AGC TTC CAG       190
Arg Pro Glu Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln
        50                  55                  60

GCC TCC GAC CCC GTT CTC ACC ATG GCC GTG GAC AGC GGA CTG AAG GAT       238
Pro Ser Asp Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp
    65                  70                  75

GAC TTG GTT TTT GGG GAC CCA AAC GCG CCG CGT TTC GTG CTG TGG GAG       286
Asp Leu Val Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu
80                  85                  90                  95

GGG AAG CTG AGG CCC GTG CCA TCC AAG CCC GCC GAC CTC CCG TTC TTC       334
Gly Lys Leu Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe
                100                 105                 110

GAT CTC ATG AGC ATC CCA GGG AAG CTC AGG GCC GGT CTA GGC GCG CTT       382
Asp Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu
            115                 120                 125

GGC ATC CGC CCG CCT CCT CCA GGC CGC GAA GAG TCA GTG GAG GAG TTC       430
Gly Ile Arg Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe
        130                 135                 140

GTG CGC CGC AAC CTC GGT GCT GAG GTC TTT GAG CGC CTC ATT GAG CCT       478
Val Arg Arg Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro
    145                 150                 155

TTC TGC TCA GGT GTC TAT GCT GGT GAT CCT TCT AAG CTC AGC ATG AAG       526
Phe Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys
160                 165                 170                 175

GCT GCA TTT GGG AAG GTT TGG CGG TTG GAA GAA ACT GGA GGT AGT ATT       574
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Ala Ala Phe Gly Lys Val Trp Arg Leu Glu Glu Thr Gly Gly Ser Ile
                180                 185                 190

ATT GGT GGA ACC ATC AAG ACA ATT CAG GAG AGG AGC AAG AAT CCA AAA      622
Ile Gly Gly Thr Ile Lys Thr Ile Gln Glu Arg Ser Lys Asn Pro Lys
            195                 200                 205

CCA CCG AGG GAT GCC CGC CTT CCG AAG CCA AAA GGG CAG ACA GTT GCA      670
Pro Pro Arg Asp Ala Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Ala
        210                 215                 220

TCT TTC AGG AAG GGT CTT GCC ATG CTT CCA AAT GCC ATT ACA TCC AGC      718
Ser Phe Arg Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser
    225                 230                 235

TTG GGT AGT AAA GTC AAA CTA TCA TGG AAA CTC ACG AGC ATT ACA AAA      766
Leu Gly Ser Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys
240                 245                 250                 255

TCA GAT GAC AAG GGA TAT GTT TTG GAG TAT GAA ACG CCA GAA GGG GTT      814
Ser Asp Asp Lys Gly Tyr Val Leu Glu Tyr Glu Thr Pro Glu Gly Val
                260                 265                 270

GTT TCG GTG CAG GCT AAA AGT GTT ATC ATG ACT ATT CCA TCA TAT GTT      862
Val Ser Val Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val
            275                 280                 285

GCT AGC AAC ATT TTG CGT CCA CTT TCA AGC GAT GCT GCA GAT GCT CTA      910
Ala Ser Asn Ile Leu Arg Pro Leu Ser Ser Asp Ala Ala Asp Ala Leu
        290                 295                 300

TCA AGA TTC TAT TAT CCA CCG GTT GCT GCT GTA ACT GTT TCG TAT CCA      958
Ser Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro
    305                 310                 315

AAG GAA GCA ATT AGA AAA GAA TGC TTA ATT GAT GGG GAA CTC CAG GGC     1006
Lys Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly
320                 325                 330                 335

TTT GGC CAG TTG CAT CCA CGT AGT CAA GGA GTT GAG ACA TTA GGA ACA     1054
Phe Gly Gln Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr
                340                 345                 350

ATA TAC AGT TCC TCA CTC TTT CCA AAT CGT GCT CCT GAC GGT AGG GTG     1102
Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Asp Gly Arg Val
            355                 360                 365

TTA CTT CTA AAC TAC ATA GGA GGT GCT ACA AAC ACA GGA ATT GTT TCC     1150
Leu Leu Leu Asn Tyr Ile Gly Gly Ala Thr Asn Thr Gly Ile Val Ser
        370                 375                 380

AAG ACT GAA AGT GAG CTG GTC GAA GCA GTT GAC CGT GAC CTC CGA AAA     1198
Lys Thr Glu Ser Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys
    385                 390                 395

ATG CTT ATA AAT TCT ACA GCA GTG GAC CCT TTA GTC CTT GGT GTT CGA     1246
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Met Leu Ile Asn Ser Thr Ala Val Asp Pro Leu Val Leu Gly Val Arg
400                 405                 410                 415

GTT TGG CCA CAA GCC ATA CCT CAG TTC CTG GTA GGA CAT CTT GAT CTT      1294
Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu
                420                 425                 430

CTG GAA GCC GCA AAA GCT GCC CTG GAC CGA GGT GGC TAC GAT GGG CTG      1342
Leu Glu Ala Ala Lys Ala Ala Leu Asp Arg Gly Gly Tyr Asp Gly Leu
            435                 440                 445

TTC CTA GGA GGG AAC TAT GTT GCA GGA GTT GCC CTG GGC AGA TGC GTT      1390
Phe Leu Gly Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Val
        450                 455                 460

GAG GGC GCG TAT GAA AGT GCC TCG CAA ATA TCT GAC TTC TTG ACC AAG      1438
Glu Gly Ala Tyr Glu Ser Ala Ser Gln Ile Ser Asp Phe Leu Thr Lys
    465                 470                 475

TAT GCC TAC AAG TGA TGAAAGAAGT GGAGCGCTAC TTGCCAATCG TTTATGTTGC      1493
Tyr Ala Tyr Lys  *
480

ATAGATGAGG TGCCTCCGGG GAAAAAAAAG CTTGAATAGT ATTTTTTATT CTTATTTTGT    1553

AAATTGCATT TCTGTTCTTT TTTCTATCAG TAATTAGTTA TATTTTAGTT CTGTAGGAGA    1613

TTGTTCTGTT CACTGCCCTT CAAAAGAAAT TTTATTTTTC ATTCTTTTAT GAGAGCTGTG    1673

CTACTTAAAA AAAAAAAAAA AAAAA                                          1698
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(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Zea mays*
- (B) STRAIN: B73 inbred

(ix) FEATURE:
- (A) NAME/KEY: peptide
- (B) LOCATION: 1..483
- (C) OTHER INFORMATION: /note="protoporphyrinogen oxidase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Asn Ser Ala Asp Cys Val Val Val Gly Gly Gly Ile Ser Gly Leu Cys
 1               5                  10                  15
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Thr Ala Gln Ala Leu Ala Thr Arg His Gly Val Gly Asp Val Leu Val
20 25 30

Thr Glu Ala Arg Ala Arg Pro Gly Gly Asn Ile Thr Thr Val Glu Arg
35 40 45

Pro Glu Glu Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro
50 55 60

Ser Asp Pro Val Leu Thr Met Ala Val Asp Ser Gly Leu Lys Asp Asp
65 70 75 80

Leu Val Phe Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Glu Gly
85 90 95

Lys Leu Arg Pro Val Pro Ser Lys Pro Ala Asp Leu Pro Phe Phe Asp
100 105 110

Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Leu Gly Ala Leu Gly
115 120 125

Ile Arg Pro Pro Pro Pro Gly Arg Glu Glu Ser Val Glu Glu Phe Val
130 135 140

Arg Arg Asn Leu Gly Ala Glu Val Phe Glu Arg Leu Ile Glu Pro Phe
145 150 155 160

Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala
165 170 175

Ala Phe Gly Lys Val Trp Arg Leu Glu Glu Thr Gly Gly Ser Ile Ile
180 185 190

Gly Gly Thr Ile Lys Thr Ile Gln Glu Arg Ser Lys Asn Pro Lys Pro
195 200 205

Pro Arg Asp Ala Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Ala Ser
210 215 220

Phe Arg Lys Gly Leu Ala Met Leu Pro Asn Ala Ile Thr Ser Ser Leu
225 230 235 240

Gly Ser Lys Val Lys Leu Ser Trp Lys Leu Thr Ser Ile Thr Lys Ser
245 250 255

Asp Asp Lys Gly Tyr Val Leu Glu Tyr Glu Thr Pro Glu Gly Val Val
260 265 270

Ser Val Gln Ala Lys Ser Val Ile Met Thr Ile Pro Ser Tyr Val Ala
275 280 285

Ser Asn Ile Leu Arg Pro Leu Ser Ser Asp Ala Ala Asp Ala Leu Ser
290 295 300

Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val Thr Val Ser Tyr Pro Lys
305 310 315 320

Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp Gly Glu Leu Gln Gly Phe
325 330 335

Gly Gln Leu His Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile
340 345 350

Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Asp Gly Arg Val Leu
355 360 365

Leu Leu Asn Tyr Ile Gly Gly Ala Thr Asn Thr Gly Ile Val Ser Lys
370 375 380

Thr Glu Ser Glu Leu Val Glu Ala Val Asp Arg Asp Leu Arg Lys Met
385 390 395 400

Leu Ile Asn Ser Thr Ala Val Asp Pro Leu Val Leu Gly Val Arg Val
405 410 415

Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu
420 425 430

Glu Ala Ala Lys Ala Ala Leu Asp Arg Gly Gly Tyr Asp Gly Leu Phe
435 440 445

Leu Gly Gly Asn Tyr Val Ala Gly Val Ala Leu Gly Arg Cys Val Glu
450 455 460

Gly Ala Tyr Glu Ser Ala Ser Gln Ile Ser Asp Phe Leu Thr Lys Tyr
465 470 475 480

Ala Tyr Lys

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: oligonucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..18
(C) OTHER INFORMATION: /note="oligonucleotide primer 1A for *Chlamydomonas reinhardtii*"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:15

CCGTCTACCA GTTTCTTG

(2) INFORMATION FOR SEQ ID NO:16

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: oligonucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..19
(C) OTHER INFORMATION: /note="oligonucleotide primer 1B for *Chlamydomonas reinhardtii*"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:16

ATACAACCGC GGGATACGA

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: oligonucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..17
(C) OTHER INFORMATION: /note="oligonucleotide primer 2A for *Chlamydomonas reinhardtii*"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:17

ACTTTGTCTG GTGCTCC

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: oligonucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..17
(C) OTHER INFORMATION: /note="oligonucleotide primer 2B for *Chlamydomonas reinhardtii*"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:18

TGGATCGCTT TGCTCAG

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULAR TYPE: DNA(genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Chlamydomonas reinhardtii*
(B) STRAIN: RS-3

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..3381
(C) OTHER INFORMATION: /note="encodes protoporphyrinogen oxidase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTCGAGAGCG TTGGAGGAAA TCCGTTTGGC ACCTGTTCCG GCTTCTTTGT GTGCACGGCC 60

ACGTCCCCCT TTCCTGCTAC CCGCTCCCCC CCGGCTTTAC TGCCCCTTCC ACTCCTCGGC 120

TCCATCCCGA TTCCATCCGC TCCTCCTCCC CCACCTAGAC TGTCTACCGT CTACCAGTTT 180

CTTGGGCAAT CATTAACGTA ACCCCGCCTC CCTGCGCCTG CCCCTCCCTC CCTCTCCCCC 240

CCGCACAGCC CGCCGCCGCC GAGGCCCTGG GCTCCTTCGA CTACCCGCCG ATGGGCGCCG 300

TGACGCTGTC GTACCCGCTG AGCGCCGTGC GGGAGGAGCG CAAGGCCTCG GACGGGTCCG 360

TGCCGGGCTT CGGTCAGCTG CACCCGCGCA CGCAGGTGGG CAAGTGCGCG CGTGTTGCGG 420

GCGGTGTGTT GCGGAGGGGA GGGTGGTGGG GGTTGGGGGT GGGGGTGGGG GGGATTGGGG 480

CGCTGGGTCG TATCCCGCGG TTGTATCCTC GCGCTCCCCT CATCCATTCC CCCCTTCAAC 540

AACACACACG GGCGCACACG CACCCTCTTT GCGCTTACTT TGTCTGGTGC TCCTTAACAC 600

ACTCTTCGCT TCATTTTGGT GTCTTCTAAC ACACACACTT GTCCACACAC AGGGCATCAC 660

CACTCTGGGC ACCATCTACA GCTCCAGCCT GTTCCCCGGC CGCGCGCCCG AGGGCCACAT 720

GCTGCTGCTC AACTACATCG GCGGCACCAC CAACCGCGGC ATCGTCAACC AGACCACCGA 780

GCAGCTGGTG GAGCAGGTGT GTGTGTGGGG GGGTGGGGGG GGGGCAGTGG ATTTTTGGGC 840

TGAGCCCCCT GAGCAAAGCG ATCCAGGGGG GGCGAAGCCC CCCAGGATTG CCCCTGTCCG 900

TGCGTGCGTG TGTGCCTGTG TCGACAAAAA GTACCGTACT GGCACAAACC GCGAGTGCCA 960

CGTATTATTA ATTGCAATTA CCTATTGTAG AAAAATAGAC GGCAGGGAAA ACTCGGCCGG 1020

AGCGAGAAGC GACCTCGTGA GTCCATGGAC ATCTTGACTT TCTTCAGTTC GCGAGTATAG 1080

CTCTCGGCCC CTAAATATCT TACATCCATG TATCAAAACA TGTCGACGAC AAGCGTCTTG 1140

GGGCAAGAAT GTCGAAATTG TTTGCAACAG CCAAACCATG CGTCCCCGAG CCTTACATGT 1200

GTCGCGGCCC GGGATCCCGC GCCCGAGCCC GGCTAGCCCT TTGCGGTGCT TGAGTGGGAT 1260

GTGGGTGAGG TGCATTTGGG ATATCATGGA CCGTGAAGTG GCGTGGGTAA GGTGGCGTGG 1320

CGTGGCGGGG ACAGGGCATG TCGGTGCCTC GGCACAGCGT TGGCCTAGTG GCCAGTCCCG 1380

CTGGATGGGC TTGCAAGGGT GCTGTTCATG TCGCCGGTGC CCATCGTCAC ATCCCCTTGC 1440

GCTACATGGG GCTCAGCCCA TTTTCCAGCT GTACAAAGCT GACACCCCTT GTTGTGTGGC 1500

GTCTTGGACC CGTGTTGCTT CGGAGCTGGC CAGAACCCCC TGTGGGCACA CACACGCACA 1560

CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA 1620

CACACACACA CACACACACA CACACACACA CACACACACA CACATTTTCG TCCTGCAGCC 1680

CCGAACCCCG CCGCCCGTTC CACGTCTTCC ACCTGCCGCA CCCCCCCCCC TGCCGCACGC 1740

CTGCTCTCAC CGCCTCTCCC CCCACCCCAT CTCCCTGCAG GTGGACAAGG ACCTGCGCAA 1800

CATGGTCATC AAGCCCGACG CGCCCAAGCC CCGTGTGGTG GGCGTGCGCG TGTGGCCGCG 1860

CGCCATCCCG CAGGTGTGAG GGCGCAGCAG CCGGAGGGAT GGGCTAGATC CTAGTTTCTC 1920

AAAGAGCTCT ACAGCCCTAT AACCTCGACC TGCGACCTTC GACCTGATAA CCTGGCTGCC 1980

CCCTCCCAAC CTAGCCACCT CTCCCCGGAT TTGGGTTCAC TCGGTTGACT TGCTTTTGGG 2040

TTCTGGAATC AACTTCACCT GTTGTATACT TTGCTGCACT TCTCTGTACC ACTCTTTGCA 2100

TTAGGTTCGG TTTAGTTTGG GCTGCATGTG TAACCCCTCC TCCCCGCCCT GCCACCTGCA 2160

GTTCAACCTG GGCCACCTGG AGCAGCTGGA CAAGGCGCGC AAGGCGCTGG ACGCGGCGGG 2220
GCTGCAGGGC GTGCACCTGG GGGGCAACTA CGTCAGCGGT GAGCGCGTGG GCAGCAGCAG 2280
CAGCAGGAAG AGGGGAGGGG AGGGGAGGGG AGGGTACAAG GAGGAGGTTG AGCAGGAGGT 2340
GGTGCTAAGG CGCAAAGCAA GGCGGTGTTG TATCCTCATT GACTGAAACC GGGAAACCCA 2400
GCATGAACAA GAGGTCAGGG GACTGCAAGG AGCGGAGGCT ACATGTATGA CTACCCCCGA 2460
CGCGGGCGAT GATTCCTTGA CTATTGGGAC CTATTTCGTT GGGCTCGGGC ACATGACCCC 2520
CCTGGCCCCT TCGCTGTATG GTGCCCAGCC GCCCAGCCGC CCCCCGCCCA CACGTGTGCC 2580
CACGCCTTTG CCTCATCCCC AACCCCCTCG GCCCCTCTCC CCCCTCGAAC CCCTGCAACC 2640
AGGTGTGGCC CTGGGCAAGG TGGTGGAGCA CGGCTACGAG TCCGCAGCCA ACCTGGCCAA 2700
GAGCGTGTCC AAGGCCGCAG TCAAGGCCTA AGCGGCTGCA GCAGTAGCAG CAGCAGCATC 2760
GGGCTGTAGC TGGTAAATGC CGCAGTGGCA CCGGCAGCAG CAATTGGCAA GCACTTGGGG 2820
CAAGCGGAGT GGAGGCGAGG GGGGGGCTAC CATTGGCGCT TGCTGGGATG TGTAGTAACA 2880
GTTGGAATGG ATCGGGGATG TGGAGCTAGG GGTTCGGGGG TCTGCCAAGG ACATAGGTGG 2940
TGCTGGGATG AGCGATGTGG TTGGTAAAGC TCTGTCGGCA CCGTTATGTG CGGGTTAACT 3000
GCACTATGAC GCTCCGTTGT ACAGCCCCGT TGTGCATTGT TTGCATGAAG TTTTGGCGAG 3060
AGTGAGTTGG CGCACACGCG GGGCGGTTTG GGGGCACTGT CCCTCAGTGT GGTCCCAGCA 3120
TAGCACAGGA GAGACACAGA ACTGAGTGAC ATAGACTAGG TCTCGAAGTA CCTTCAAAAG 3180
GGGGCTATAA ATTGCGAATA CCCGGAGCAG GGGGCCAGAC CCAAGGCATT GACTGTCAGT 3240
GCACAAGCGA AAGACCAATT GCATGGGTTG CTTCCGTGGT GGGAAGAGGA GGGCAGGGGA 3300
GCATCGTCAG GTGTATGTTG CGGCTTCGCC CATAAGTGCC ATGGTTTCGA AGATGCTTAA 3360
GACTAACAAT GCCAACTCGA G 3381

(2) INFORMATION FOR SEQ ID NO:20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: oligonucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..18
(C) OTHER INFORMATION: /note="oligonucleotide primer 3A for Chlamydomonas reinhardtii"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:20

TTCCACGTCT TCCACCTG

(2) INFORMATION FOR SEQ ID NO:21

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: oligonucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..17
(C) OTHER INFORMATION: /note="oligonucleotide primer 3B for *Chlamydomonas reinhardtii*"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:21

CTAGGATCTA GCCCATC

(2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: oligonucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..18
(C) OTHER INFORMATION: /note="oligonucleotide primer 4A for *Chlamydomonas reinhardtii*"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:22

CTGCATGTGT AACCCCTC

(2) INFORMATION FOR SEQ ID NO:23

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: oligonucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..18
(C) OTHER INFORMATION: /note="oligonucleotide primer 4B for *Chlamydomonas reinhardtii*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

GACCTCTTGT TCATGCTG

(2) INFORMATION FOR SEQ ID NO:24

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: oligonucleotide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..17
(C) OTHER INFORMATION: /note="oligonucleotide primer 5B for *Chlamydomonas reinhardtii*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

CGGCATTTAC CAGCTAC